



P# 9

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/654,281

Source: 1642

Date Processed by STIC: 5-14-01

RECEIVED

MAY 31 2001

TECH CENTER 1600.2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED CORRECTION

SERIAL NUMBER: 09/654,281

ATTN: NEW-RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE.

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- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
  
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
  
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
  
- 6 ☒ Variable Length      Sequence(s) 1, possibly more contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.  
<221>
  
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
  
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
  
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 11 ☒ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
  
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
  
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1642

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/654,281

DATE: 05/14/2001  
 TIME: 12:18:24

Input Set : A:\ES.txt  
 Output Set: N:\CRF3\05142001\I654281.raw

Does Not Comply  
 Corrected Diskette Needed  
 pp 1-2, 5

3 <110> APPLICANT: Sedivy, John  
 4 Kolch, Walter  
 5 Yeung, Kam Chi  
 7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and Modulation  
 8 of Cell Proliferation and Growth  
 10 <130> FILE REFERENCE: 3564/1010  
 12 <140> CURRENT APPLICATION NUMBER: 09/654,281  
 13 <141> CURRENT FILING DATE: 2000-09-01  
 15 <150> PRIOR APPLICATION NUMBER: 60/151,992  
 16 <151> PRIOR FILING DATE: 1999-09-01  
 18 <160> NUMBER OF SEQ ID NOS: 11  
 20 <170> SOFTWARE: PatentIn version 3.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 42  
 24 <212> TYPE: PRT  
 C--> 25 <213> ORGANISM: Artificial  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: consensus sequence  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: UNSURE  
 32 <222> LOCATION: (3)..(5)  
 33 <223> OTHER INFORMATION: Xaa = any amino acid  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: UNSURE  
 38 <222> LOCATION: (9)..(9)  
 39 <223> OTHER INFORMATION: a hydrophobic amino acid residue  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: UNSURE  
 44 <222> LOCATION: (11)..(13)  
 45 <223> OTHER INFORMATION: Xaa = any amino acid  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: UNSURE  
 50 <222> LOCATION: (14)..(14)  
 51 <223> OTHER INFORMATION: a negatively charged amino acid residue  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: UNSURE  
 56 <222> LOCATION: (15)..(18)  
 57 <223> OTHER INFORMATION: Xaa = any amino acid residue  
 60 <220> FEATURE:  
 61 <221> NAME/KEY: UNSURE  
 62 <222> LOCATION: (20)..(21)  
 63 <223> OTHER INFORMATION: Xaa = any amino acid residue  
 66 <220> FEATURE:  
 67 <221> NAME/KEY: UNSURE  
 68 <222> LOCATION: (23)..(23)  
 69 <223> OTHER INFORMATION: Xaa = 50 of any amino acid residue, 0 to 40 residues may be missi  
 70 n

Incomplete <213> response as  
 per section 1.823b of new  
 sequence rules. See #11 on the  
 Error Summary sheet.

Note: This error is also  
 indicated in sequence  
 #'s 10 and 11. Please  
 review and correct.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/654,281

DATE: 05/14/2001  
TIME: 12:18:24

Input Set : A:\ES.txt  
Output Set: N:\CRF3\05142001\I654281.raw

```

73 <220> FEATURE:
74 <221> NAME/KEY: UNSURE
75 <222> LOCATION: (25)..(28)
76 <223> OTHER INFORMATION: Xaa = any amino acid residue
79 <220> FEATURE:
80 <221> NAME/KEY: UNSURE
81 <222> LOCATION: (30)..(30)
82 <223> OTHER INFORMATION: Xaa = 4 of any amino acid residue, 0 to 2 residues may be missing
85 <220> FEATURE:
86 <221> NAME/KEY: UNSURE
87 <222> LOCATION: (32)..(32)
88 <223> OTHER INFORMATION: Xaa = any amino acid residue
91 <220> FEATURE:
92 <221> NAME/KEY: UNSURE
93 <222> LOCATION: (35)..(35)
94 <223> OTHER INFORMATION: Xaa = an aromatic amino acid residue
97 <220> FEATURE:
98 <221> NAME/KEY: UNSURE
99 <222> LOCATION: (37)..(37)
100 <223> OTHER INFORMATION: Xaa = any amino acid residue
103 <220> FEATURE:
104 <221> NAME/KEY: UNSURE
105 <222> LOCATION: (38)..(38)
106 <223> OTHER INFORMATION: a hydrophobic amino acid residue
109 <220> FEATURE:
110 <221> NAME/KEY: UNSURE
111 <222> LOCATION: (39)..(41)
112 <223> OTHER INFORMATION: Xaa = any amino acid residue
115 <400> SEQUENCE: 1
W--> 117 Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
      118 1 5 10 15
W--> 120 Xaa Xaa Glu Xaa Xaa His Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Gly Xaa
      121 20 25 30
W--> 123 His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
      124 35 40
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 187
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 2
133 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
134 1 5 10 15
136 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
137 20 25 30
139 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
140 35 40 45
142 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
143 50 55 60
145 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys

```

"Xaa's" at positions  
23 + 30 have variable  
length error. Each  
Xaa may only represent  
one residue. See  
# 6 on the Error  
Summary sheet.

## RAW SEQUENCE LISTING

DATE: 05/14/2001

PATENT APPLICATION: US/09/654,281

TIME: 12:18:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\05142001\I654281.raw

```

146 65          70          75          80
148 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
149          85          90          95
151 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
152          100          105          110
154 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
155          115          120          125
157 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
158          130          135          140
160 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
161 145          150          155          160
163 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
164          165          170          175
166 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
167          180          185
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 187
171 <212> TYPE: PRT
172 <213> ORGANISM: Mus musculus
174 <220> FEATURE:
175 <221> NAME/KEY: UNSURE
176 <222> LOCATION: (150)..(150)
177 <223> OTHER INFORMATION: Xaa = any amino acid residue
180 <400> SEQUENCE: 3
182 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
183 1          5          10          15
185 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
186          20          25          30
188 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
189          35          40          45
191 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
192          50          55          60
194 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
195 65          70          75          80
197 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
198          85          90          95
200 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
201          100          105          110
203 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
204          115          120          125
206 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
207          130          135          140
W--> 209 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
210 145          150          155          160
212 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
213          165          170          175
215 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
216          180          185
218 <210> SEQ ID NO: 4

```

## RAW SEQUENCE LISTING

DATE: 05/14/2001

PATENT APPLICATION: US/09/654,281

TIME: 12:18:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\05142001\I654281.raw

219 &lt;211&gt; LENGTH: 187

220 &lt;212&gt; TYPE: PRT

221 &lt;213&gt; ORGANISM: Drosophila

223 &lt;400&gt; SEQUENCE: 4

```

225 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
226 1 5 10 15
228 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
229 20 25 30
231 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
232 35 40 45
234 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
235 50 55 60
237 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
238 65 70 75 80
240 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
241 85 90 95
243 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
244 100 105 110
246 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
247 115 120 125
249 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
250 130 135 140
252 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
253 145 150 155 160
255 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
256 165 170 175
258 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
259 180 185

```

261 &lt;210&gt; SEQ ID NO: 5

262 &lt;211&gt; LENGTH: 220

263 &lt;212&gt; TYPE: PRT

264 &lt;213&gt; ORGANISM: C. elegans

266 &lt;400&gt; SEQUENCE: 5

```

268 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
269 1 5 10 15
271 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
272 20 25 30
274 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
275 35 40 45
277 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys
278 50 55 60
280 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
281 65 70 75 80
283 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
284 85 90 95
286 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
287 100 105 110
289 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
290 115 120 125

```

## RAW SEQUENCE LISTING

DATE: 05/14/2001

PATENT APPLICATION: US/09/654,281

TIME: 12:18:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\05142001\I654281.raw

```

292 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
293      130      135      140
295 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln
296 145      150      155      160
298 Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
299      165      170      175
301 Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
302      180      185      190
304 Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
305      195      200      205
307 Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
308      210      215      220
310 <210> SEQ ID NO: 6
311 <211> LENGTH: 181
312 <212> TYPE: PRT
313 <213> ORGANISM: Antirrhinum-CEN
315 <400> SEQUENCE: 6
317 Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile
318 1      5      10      15
320 Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
321      20      25      30
323 Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
324      35      40      45
326 Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
327      50      55      60
329 Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
330 65      70      75      80
332 Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
333      85      90      95
335 Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
336      100      105      110
338 Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
339      115      120      125
341 Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
342      130      135      140
344 Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
345 145      150      155      160
347 Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
348      165      170      175
350 Ala Ala Arg Arg Arg
351      180
353 <210> SEQ ID NO: 7
354 <211> LENGTH: 176
355 <212> TYPE: PRT
356 <213> ORGANISM: Arabidopsis-TFL1
358 <400> SEQUENCE: 7
360 Met Glu Asn Met Gly Thr Arg Val Ile Glu Pro Leu Ile Met Gly Arg
361 1      5      10      15
363 Val Val Gly Asp Val Leu Asp Phe Phe Thr Pro Thr Thr Lys Met Asn

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

F. 4. 1. →

VERIFICATION SUMMARY                      DATE: 05/14/2001  
PATENT APPLICATION:    US/09/654,281              TIME: 12:18:25

Input Set : A:\ES.txt  
Output Set: N:\CRF3\05142001\I654281.raw

L:25 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:460 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:480 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11